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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Wed Jun 06 10:07:03 EDT 2007

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Application No: 10588555 Version No: 1.1

Input Set:

Output Set:

**Started:** 2007-06-06 10:06:46.807  
**Finished:** 2007-06-06 10:06:50.515  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 708 ms  
**Total Warnings:** 2  
**Total Errors:** 975  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 323	Invalid/missing amino acid numbering in SEQID (1) POS (328)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (5)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (10)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (15)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (20)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (25)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (30)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (35)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (40)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (45)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (50)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (55)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (60)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (65)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (70)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (75)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (80)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (85)
E 323	Invalid/missing amino acid numbering SEQID (2) POS (90)

**Input Set:**

**Output Set:**

**Started:** 2007-06-06 10:06:46.807  
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Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (2)at Protein (94) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
E 341	'Xaa' position not defined SEQID (16) POS (96)
E 341	'Xaa' position not defined SEQID (16) POS (226)
E 341	'Xaa' position not defined SEQID (16) POS (233)
E 341	'Xaa' position not defined SEQID (16) POS (268)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

# SEQUENCE LISTING

<110> Svendsen, Allan  
Minning, Stefan

<120> Protease Variants

<130> 10517.204-US

<140> 10588555

<141> 2007-06-01

<160> 18

<170> PatentIn version 3.3

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<212> DNA

<213> Bacillus licheniformis

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ggg att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca	96
Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro	
-75 -70 -65	

tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca	144
Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr	
-60 -55 -50	

tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat	192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr	
-45 -40 -35	

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Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys	

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gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg				288
Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val				
	-10	-5	-1 1	
att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg				336
Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro				
	5	10	15	
tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga				384
Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly				
	20	25	30	
tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat				432
Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr				
	35	40	45 50	
gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga				480
Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly				
	55	60	65	
cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac				528
Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr				
	70	75	80	
ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga				576
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly				
	85	90	95	
gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga				624
Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly				
	100	105	110	
tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc				672
Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser				
	115	120	125 130	
ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga				720
Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly				
	135	140	145	
ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg				768
Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr				
	150	155	160	
tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga				816
Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg				
	165	170	175	
acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta				864
Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val				
	180	185	190	
tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg				912
Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val				
	195	200	205 210	

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948

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-75 -70 -65

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr  
-60 -55 -50

Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr  
-45 -40 -35

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys  
-30 -25 -20 -15

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val  
-10 -5 -1 1

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro  
5 10 15

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly  
20 25 30

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr  
35 40 45 50

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly  
55 60 65

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr  
70 75 80

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly  
85 90 95

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly  
100 105 110

Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser  
115 120 125 130

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly  
135 140 145

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr  
150 155 160

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg  
165 170 175

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val  
180 185 190

Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val  
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Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln  
215 220

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agt ggg att cta tcc cca gta aac gca act caa gct gag act ctt act	93
Ser Gly Ile Leu Ser Pro Val Asn Ala Thr Gln Ala Glu Thr Leu Thr	
-105 -100 -95 -90	
aaa tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat	141
Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp	
-85 -80 -75	
gaa gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg	189
Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser	
-70 -65 -60	
att att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act	237
Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr	
-55 -50 -45	
tct tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa	285
Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu	
-40 -35 -30	
gaa ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag	333
Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys	
-25 -20 -15 -10	
cct att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg	381
Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly	
-5 -1 1 5	
aga aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act	429
Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr	
10 15 20	
tat att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt	477
Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly	
25 30 35	
gtg att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt	525
Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly	
40 45 50 55	
tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg	573
Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp	
60 65 70	
gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac	621
Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr	
75 80 85	
aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca	669
Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala	
90 95 100	



cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct	717
Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser	
105 110 115	

ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat	765
Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr	
120 125 130 135	

gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg	813
Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp	
140 145 150	

gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc	861
Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe	
155 160 165	

tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac	909
Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn	
170 175 180	

agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt	957
Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly	
185 190 195	

ggg aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca	1005
Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr	
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Asn Leu Phe Asn Gln Met Asn	
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-105 -100 -95 -90

Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
-85 -80 -75

Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
-70 -65 -60

Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr  
-55 -50 -45

Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu  
-40 -35 -30

Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys  
-25 -20 -15 -10

Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly  
-5 -1 1 5

Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr  
10 15 20

Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly  
25 30 35

Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly  
40 45 50 55

Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp  
60 65 70

Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr  
75 80 85

Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala  
90 95 100

Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser  
105 110 115

Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr  
120 125 130 135

Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp  
140 145 150

Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe  
155 160 165

Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn

170

175

180

Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly  
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Asn Leu Phe Asn Gln Met Asn  
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att tct att ttt tct tcg ggc att tac tct gca caa gct gca tca tcg 96

Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser  
 -75 -70 -65

ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144

Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr  
 -60 -55 -50 -45

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Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala  
 -40 -35 -30

ttc gaa gga acc gga aca ccc ggc ggc tcc gtt cag gcc aaa ccg aaa 240

Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys  
 -25 -20 -15

aaa gaa tcg ccc gcc ggc ccg cct tac agc cct aaa tcg gta atc ggc	288
Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly	
-10 -5 -1 1	
tca gat gaa cgg aca agg gtg act gat aca acg gcc ttt cca tac aga	336